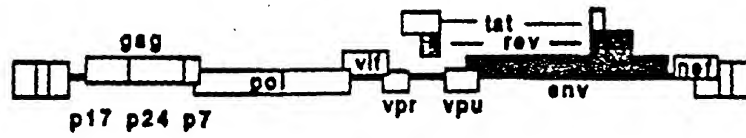


A



B

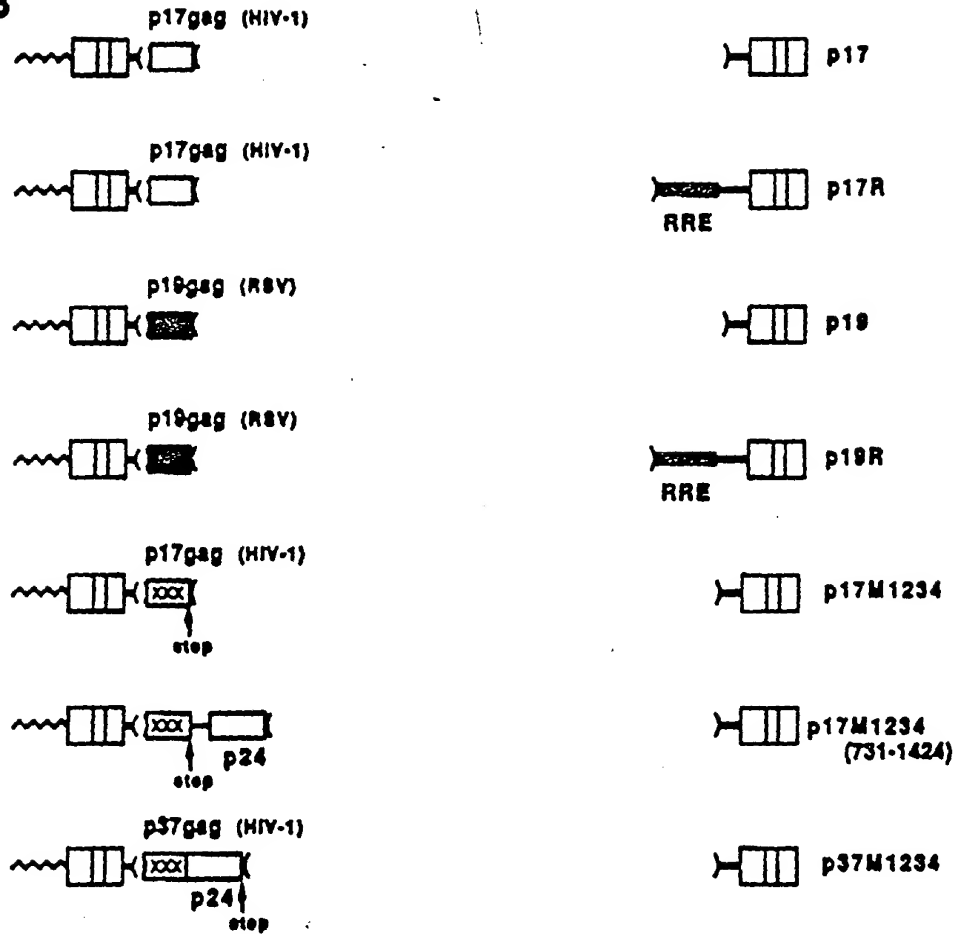
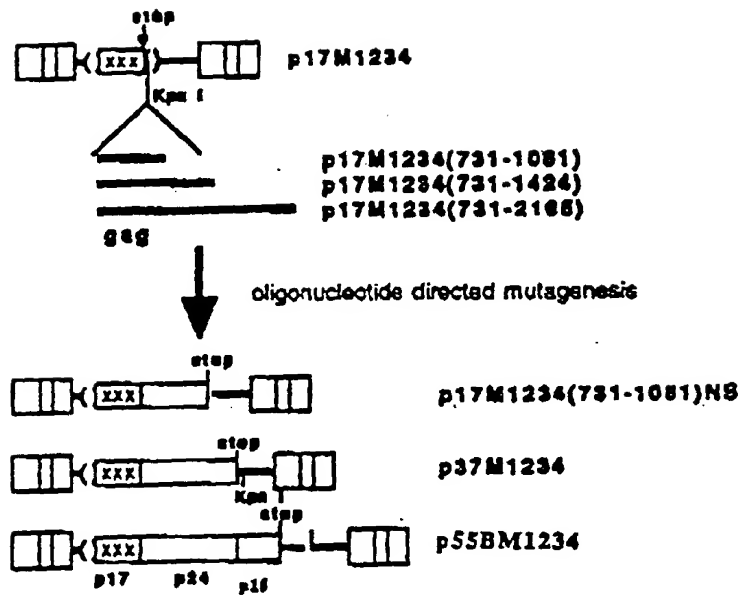


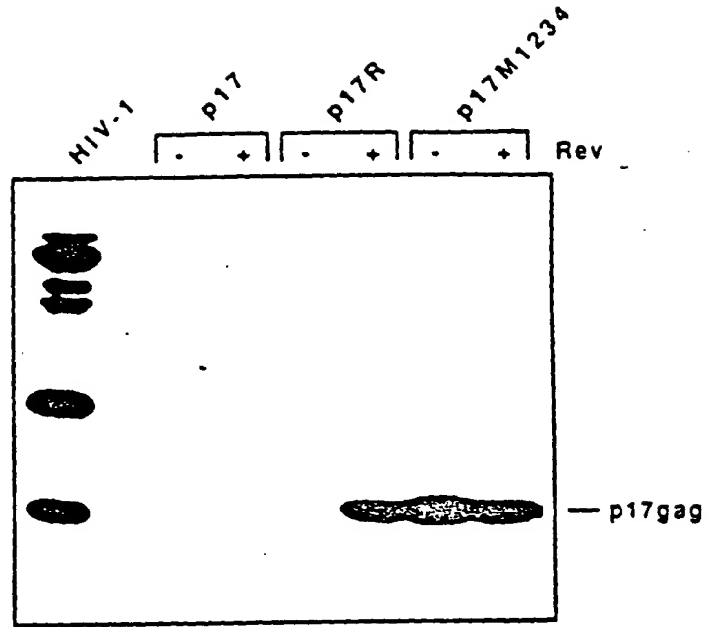
Fig. 1

c

Fig. 1 <sup>^</sup> continued

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A



B

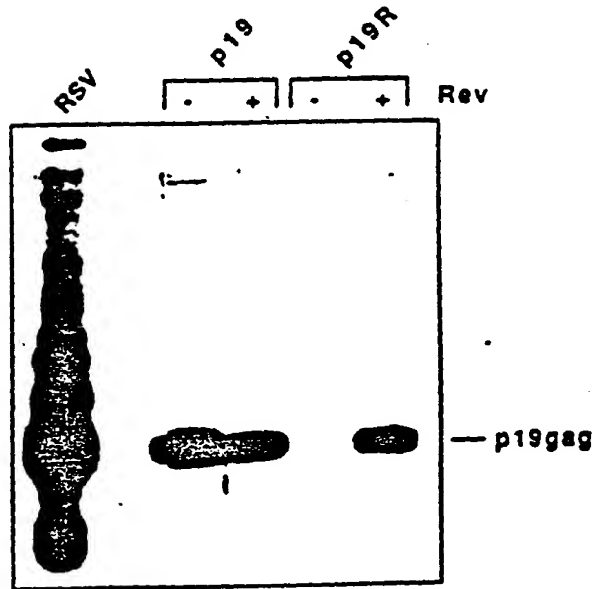
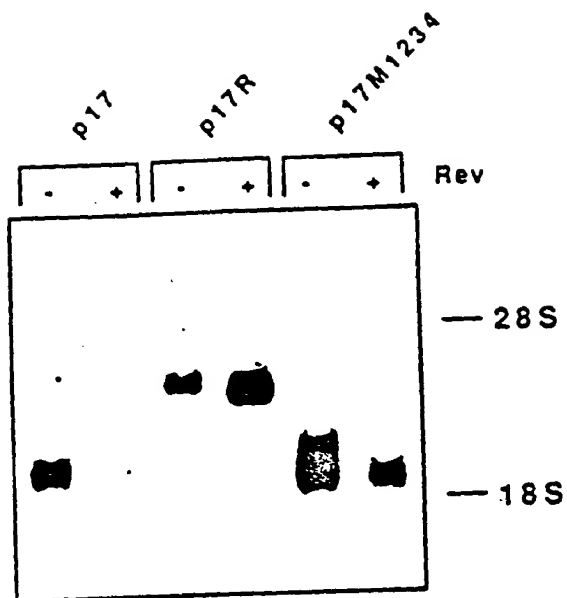


Fig. 2

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A



B

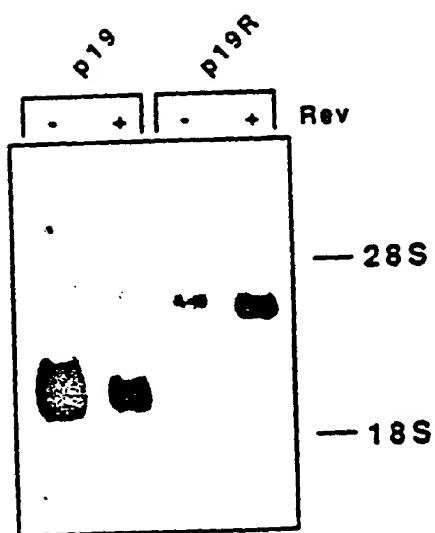


Fig. 3

Fig. 4

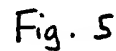
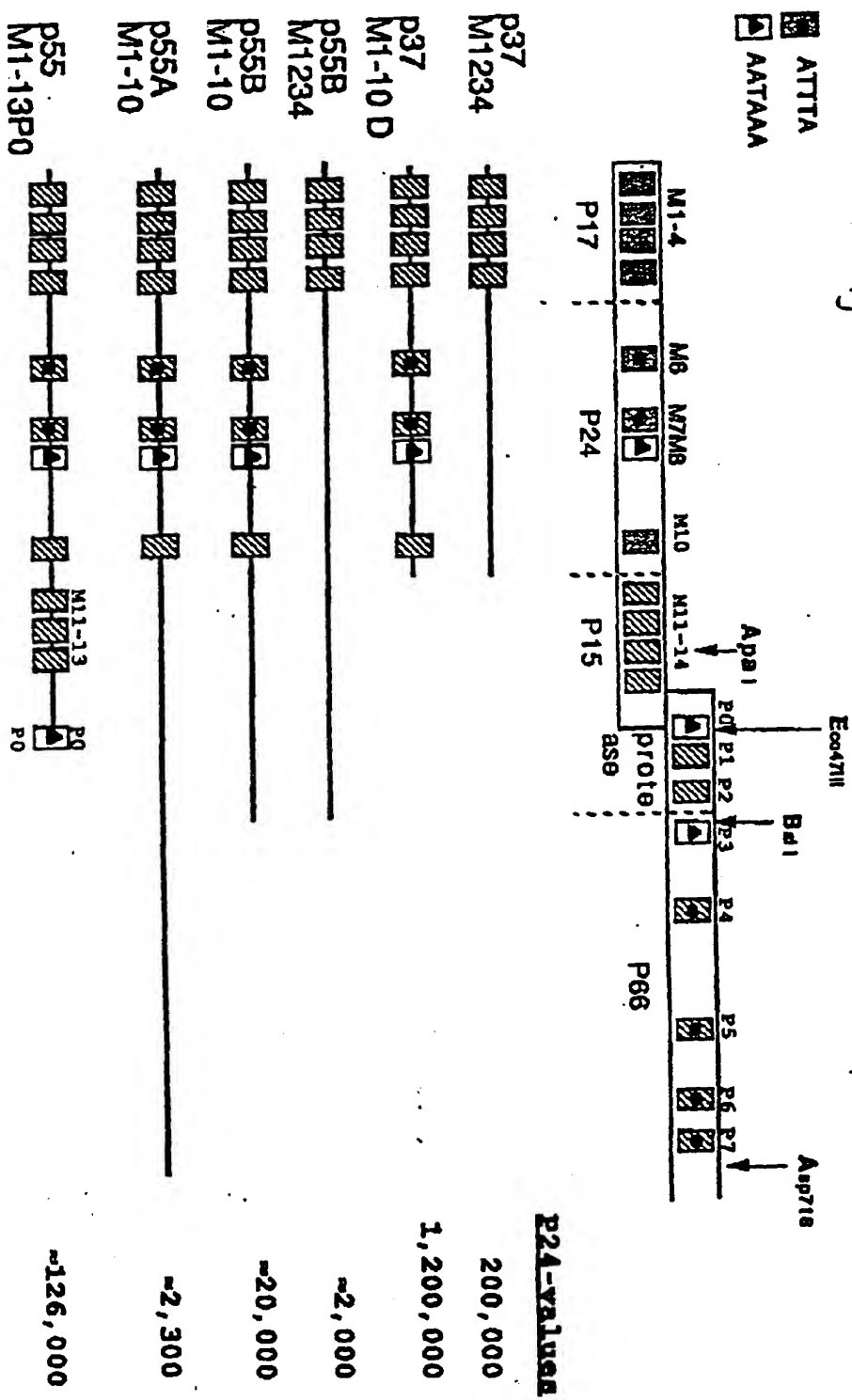


Fig. 6



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00043722-003474

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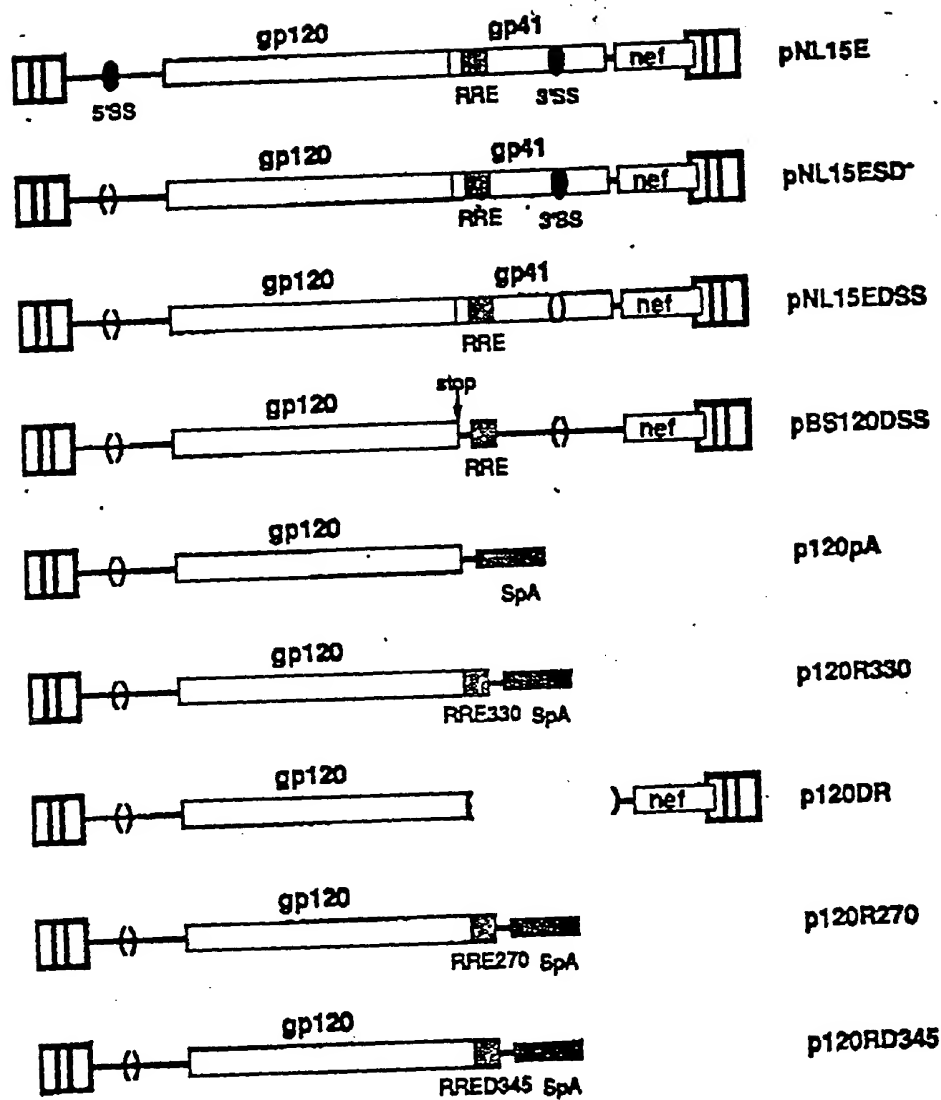
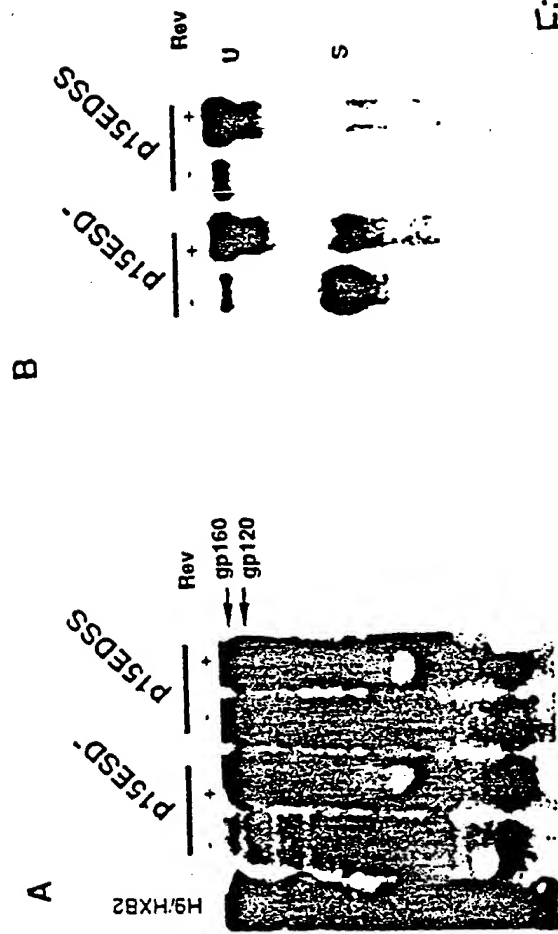
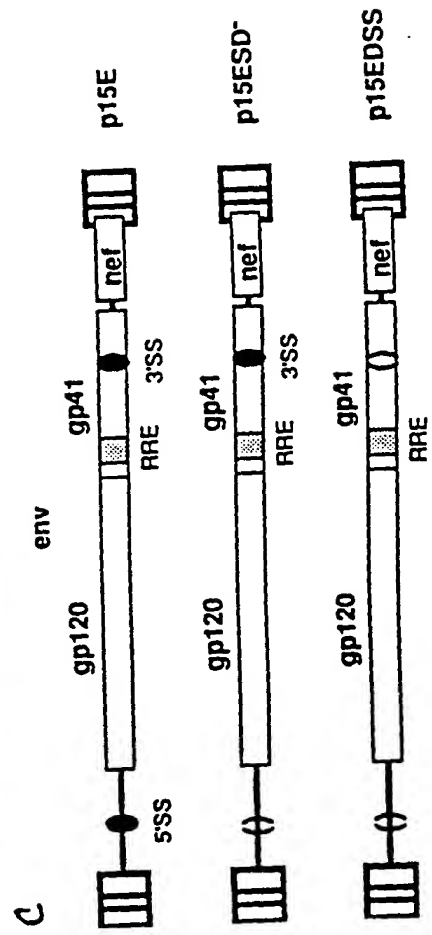


Fig. 7



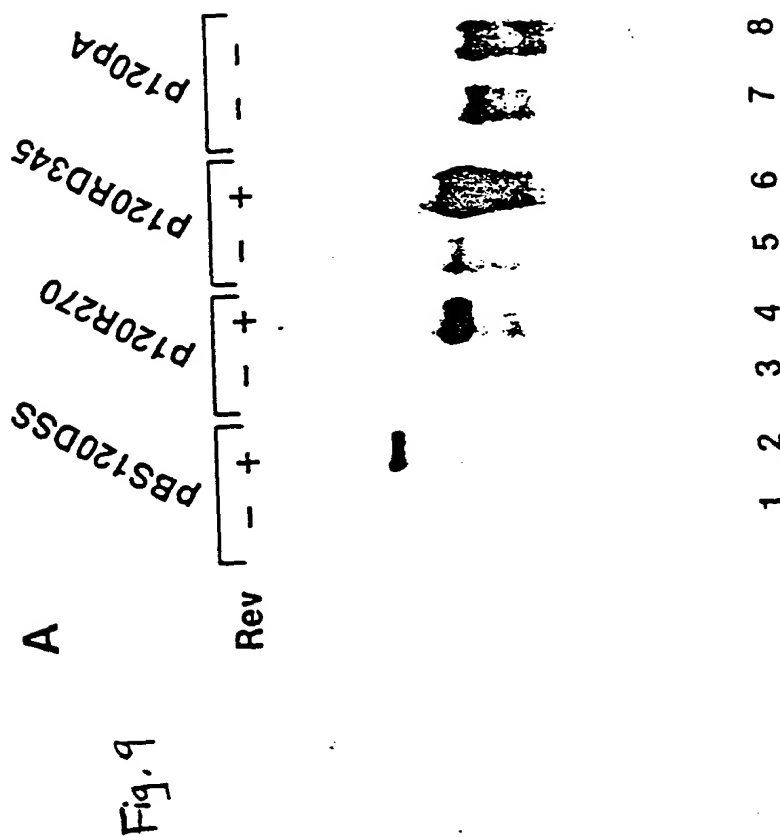
8.  
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101600 2221600



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70600 226000

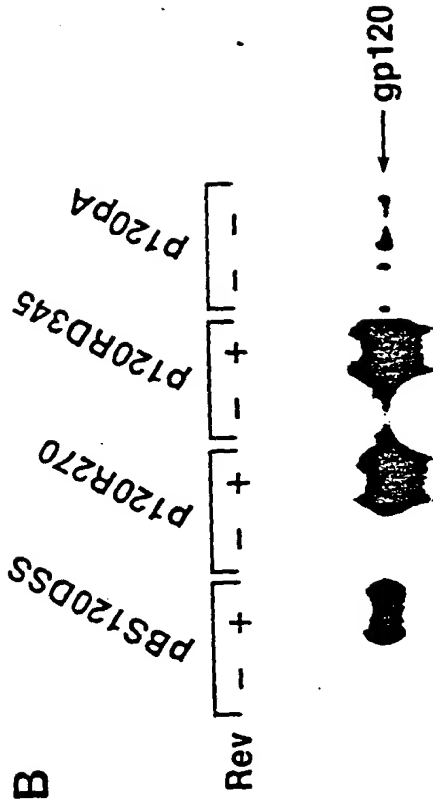
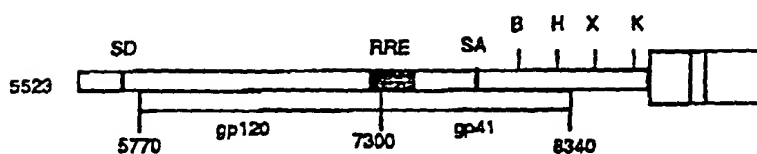


Fig. 9

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# Identification of INS regions within the env mRNA using the p19 vector.



FRAGMENT SIZE		INS EFFECT	
A	276	7684-7859	none
B	234	7684-7884, 7927-7959	none
C	323	7595-7884, 7927-7959	10 X
D	128	7939-8066	none
E	478	7939-8418	10 X
F	362	8220-8581	> 100 X
G	330	7266-7595	3-5X
E	668	5523-8190	10 X

Fig. 10

# Identification of INS regions within the env mRNA using the p37M1-10D vector.

(fig 5 env,  
formerly fig D)

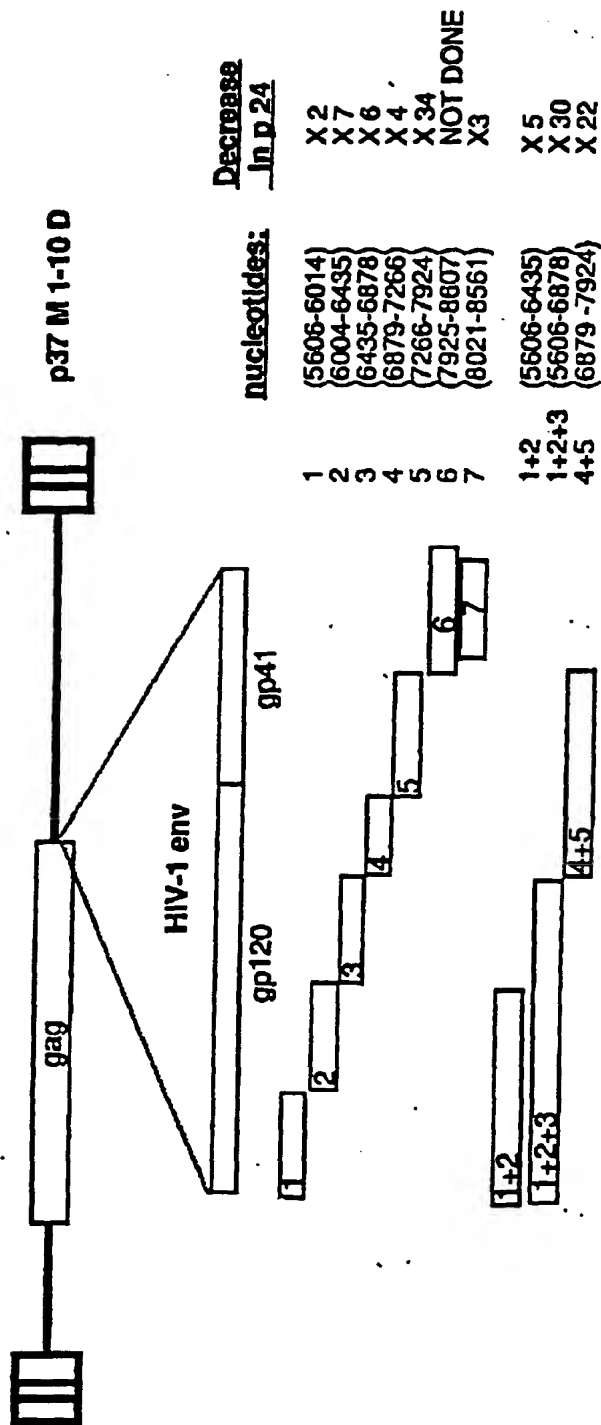
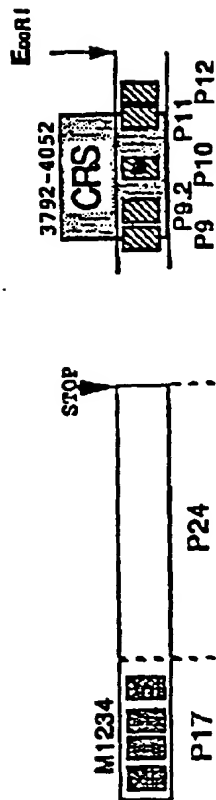


Fig. 11

# Elimination of negative effects of CRS

ATTIA



level of P24  
expression

p37M1234	100 %
p37M1234RCRS	12 %
p37M1234RCRSP10	10 %
p37M1234RCRSP12	11 %
p37M1234RCRSP10+P12p	96 %

Fig. 12

1418

Sub  
B4

POINT MUTATIONS ELIMINATING THE NEGATIVE EFFECTS OF CRS IN THE pol REGION  
(nucleotides 3700-4194)

GGTACCAGCACACAAGGAATTGGAGGAATGAACAAGTAGATAAATTAGTCAGTCTGGAAATCAGGAAGTACTATTTT  
TAGATGGAATAGATAAGGCCCAAGATGAACATGAGAATATATCACAGTAATTGGAGAGCAATGGCTAGTGATTTTAACCTG  
CCACCTGTAGTAGCAAAAGAATAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAGGCCATGCATGGACAAGTAGA  
CTGTAGTCCAGGAATATGGCAACTAGATTGTACACATTTAGAGGAAAAGTTATCCTGGTAGCAGTTCATGTAGCCAGTG  
GATATATAGAACGACAGAGTTATTCCAGCAGAAAACAGGGCAGGAAACACAGCATATTTCTTTTAAAATTAGCAGGAAGATGG  
CCAGTAAAACAATACATACACTGACAAATGGCAGCAATTTACCCGGTGTACGGTTAGGGCCCTGTGGTGGGGGGGAAT  
CAAGCAGGAATTTGG

Fig. 13

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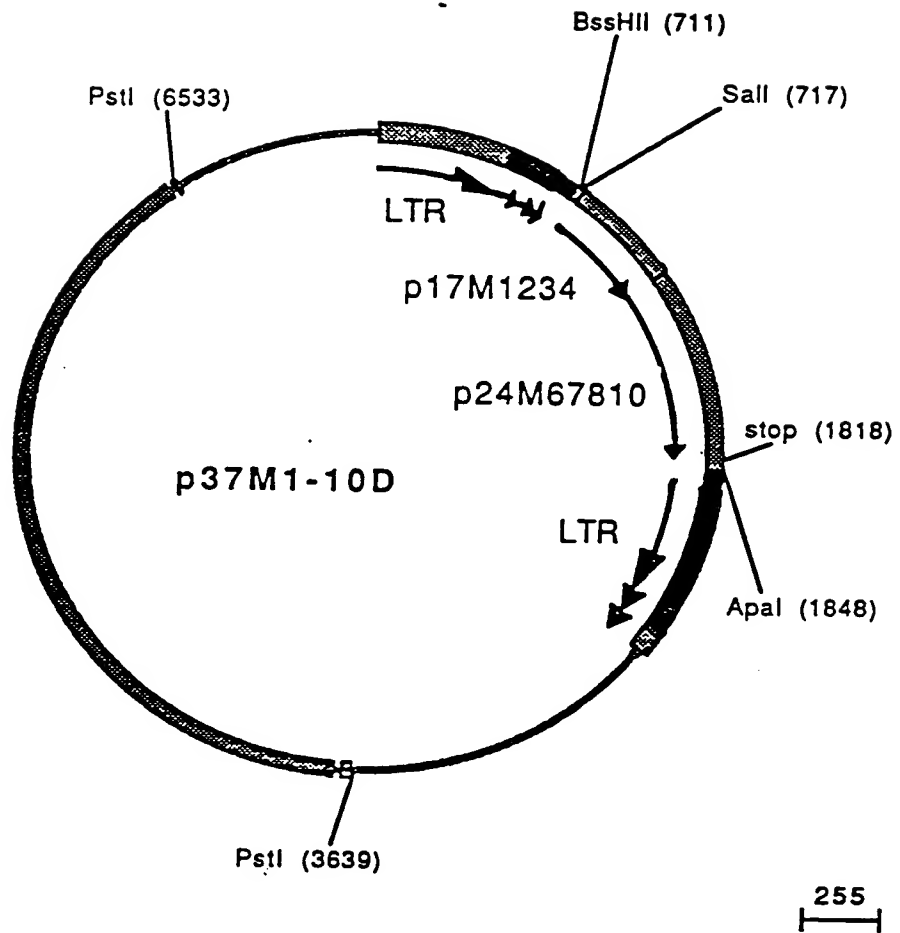


Fig. 14

A

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INS  
B5

1 TGGAGGGCT AATTTGGTCC CAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA CACAAGGCTA  
 71 CTTCCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC TGACCTTTGG ATGGTGCTTC  
 141 AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA AATAAGGAGA GAAGAACAGC TTGTTACACC  
 211 CTATGAGCCA GCATGGGATG GAGGACCCGG AGGGAGAAGT ATTAGTGTGG AAGTTTGACA GCCTCCTAGC  
 281 ATTCGTACAC ATGGCCCGAG AGCTGCATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG  
 351 GGACTTTCCG CTGGGGACTT TCCAGGGAGG TGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT  
 421 GCTACATATA AGCAGCTGCT TTTTGCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA GCCTGGGAGC  
 491 TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCCT TGAGTGTCTA AAGTAGTGTG  
 561 TGCCCGTCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC AGACCTTTT AGTCAGTGTG GAAAATCTCT  
 631 AGCAGTGGCG CCCGAACAGG GACTTGAAAG CGAAAGTAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG  
 BssHII (711)  
 701 GCTTGCTGAAGCGCGCTCGACAGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGAGAATTAGATCGATGG  
 1 Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Gly Leu Asp Arg Trp  
 777 GAAAAAATTCGGTTAAGGCCAGGGGGAAAGAAGTACAAGCTAAAGCACATCGTATGGGCAAGCAGGGAGCTAG  
 17 Gly Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Gly Leu G  
 853 AACGATTGCGAGTTAATCCTGGCCTGTTAGAACATCAGAAGGCTGTAGACAAATACTGGGACAGCTACAACCATC  
 42 Leu Arg Phe Ala Val Asn Pro Gly Leu Leu Gly Thr Ser Gly Cys Arg Gly Ile Leu Gly Gly Leu Gly n Pro Se  
 929 CCTTCAGACAGGATCAGAGGAGCTTCGATCACTATACAACACAGTAGCAACCTCTATTGTGTGCACCAGCGGATC  
 67 Leu Gly n Thr Gly Ser Gly Gly Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gly n Arg Ile  
 1005 GAGATCAAGGACACCAAGGAAGCTTTAGACAAGATAGAGGAAGAGCAAAACAAGTCCAAGAAGAAGGCCAGCAGG  
 93 Gly Ile Lys Asp Thr Lys Gly Ala Leu Asp Lys Ile Gly Gly Gly n Asn Lys Ser Lys Lys Lys Ala Gly n Gl n A  
 1081 CAGCAGCTGACACAGGACACAGCAATCAGGTGAGCCAAAATTACCCTATAGTGCAGAACATCCAGGGGCAATGGT  
 118 Ala Ala Asp Thr Gly His Ser Asn Gly n Val Ser Gly n Asn Thr Pro Ile Val Gly n Asn Ile Gly n Gly n Met Val  
 1157 ACATCAGGCCATATCACCTAGAACTTTAAATGCATGGGTAAAAGTAGTAGAAGAGAAGGCTTTTCAGCCCAGAAGTG  
 11 His Gly n Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Gly Gly Lys Ala Phe Ser Pro Gly n Val  
 1233 ATACCCATGTTTTCAGCATTATCAGAAGGAGCCACCCACAGGACCTGAACACGATGTTGAACACCGTGGGGGGAC  
 37 Ile Pro Met Phe Ser Ala Leu Ser Gly Gly Ala Thr Pro Gly n Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly H  
 1309 ATCAAGCAGCCATGCAATGTTAAAAGAGACCATCAATGAGGAAGCTGCAGAAATGGGATAGAGTGCATCCAGTGCA  
 62 Is Gly n Ala Ala Met Gly n Met Leu Lys Gly Thr Ile Asn Gly n Gly n Ala Ala Gly n Trp Asp Arg Val His Pro Val His  
 1385 TGCAGGGCCTATTGCACCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCAGGAAGTACTAGTACCCCTTCAG  
 87 Ala Gly Pro Ile Ala Pro Gly Gly n Met Arg Gly n Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gly n  
 1461 GAACAAATAGGATGGATGACAAATAATCCACCTATCCAGTAGGAGAGATCTACAAGAGGTGGATAATCCTGGGAT  
 113 Gly n Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Gly Ile Tyr Lys Arg Trp Ile Ile Leu Gly L  
 1537 TGAACAAGATCGTGAGGATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAGGAACCCCTTAGAGA  
 138 Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gly n Gly Pro Lys Gly n Pro Phe Arg As

Fig. 14 B

Continued



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1613 CTATGTAGACCGGTTCTATAAACTCTAAGAGCTGAGCAAGCTTCACAGGAGGTAAAAAATTGGATGACAGAAACC  
 163 pTyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnGluValLysAsnTrpMetThrGluThr

1689 TTGTTGGTCCAAAATGCCAACCAGATTGTAAGACCATCCTGAAGGCTCTCGGCCAGCGGCTACACTAGAAGAA  
 189 LeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLysAlaLeuGlyProAlaAlaThrLeuGluGluM

1765 TGATGACAGCATGTGAGGGAGTAGGAGGACCCGGCCATAAGGCAAGAGTTTTGTAGGGATCCACTAGTTCTAGACT  
 214 e1MetThrAlaCysGlnGlyValGlyGlyProGlyHisLysAlaArgValLeu

stop (1818)

XbaI (1838)

ApaI (1848)

1841 CGAGGGGGGG CCCGGTACCT TTAAGACCAA TGACTTACAA GGCAGCTGTA GATCTTAGCC ACTTTTAA

1911 AGAAAAGGGG GGAAGTGAAG GGCTAATTCA CTCCAAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC

1981 CACACACAAG GCTACTTCCC TGATTGGCAG AACTACACAC CAGGGCCAGG GGTCAGATAT CCACTGACCT

2051 TTGGATGGTG CTACAAGCTA GTACCAGTTG AGCCAGATAA GGTAAGAGAG GCCAATAAAG GAGAGAACAC

2121 CAGCTTGITA CACCTGTGA GCCTGCATGG AATGGATGAC CCTGAGAGAG AAGTGTTAGA GTGGAGGTTT

2191 GACAGCCGCC TAGCATTTCA TCACGTGGCC CGAGAGCTGC ATCCGGAGTA CTTCAAGAAC TGCTGACATC

2261 GAGCTTGCTA CAAGGGACTT TCCGCTGGGG ACTTCCAGG GAGGCGTGGC CTGGGCGGGA CTGGGGAGTG

2331 GCGAGCCCTC AGATGCTGCA TATAAGCAGC TGCTTTTTGC CTGTACTGGG TCTCTCTGGT TAGACCAGAT

2401 CTGAGCCTGG GAGCTCTCTG GCTAACTAGG GAACCCACTG CTTAAGCCTC AATAAAGCTT GCCTTGAGTG

2471 CTTCAAGTAG TGTGTGCCCC TCTGTTGTGT GACTCTGGTA ACTAGAGATC CCTCAGACCC TTTTAGTCAG

2541 TGTGGAATA CTCTAGCACC CCCAGGAGG TAGAGGTTGC AGTGAGCCAA GATCGCGCCA CTGCATTCCA

2611 GCCTGGGCAA GAAAACAAGA CTGTCTAAAA TAATAATAAT AAGTTAAGGG TATTAAATAT ATTTATACAT

2681 GGAGGTCATA AAAATATATA TATTTGGGCT GGGCGCAGTG GCTCACACCT GCGCCCGGCC CTTTGGGAGG

2751 CCGAGGCAGG TGGATCACCT GAGTTTGGGA GTTCCAGACC AGCCTGACCA ACATGGAGAA ACCCCTTCTC

2821 TGTGTATTTT TAGTAGATT TATTTTATGT GTATTTTATT CACAGGTATT TCTGGAAAAC TGAAACTGTT

2891 TTTCTCTAC TCTGATACCA CAAGAATCAT CAGCAGAGAG GAAGACTTCT GTGATCAAAT GTGGTGGGAG

2961 AGGGAGGTTT TCACCAGCAC ATGAGCAGTC AGTTCGTCGG CAGACTCGGC GGGTGTCTCT CGGTTCAGTT

3031 CCAACACCGC CTGCCTGGAG AGAGGTCAGA CCACAGGGTG AGGGCTCAGT CCCCAGACA TAAACACCCA

3101 AGACATAAAC ACCCAACAGG TCCACCCCGC CTGCTGCCCA GGCAGAGCCG ATTCACCAAG ACGGGAATTA

3171 GGATAGAGAA AGAGTAAGTC ACACAGAGCC GGCTGTGCGG GAGAACGGAG TTCTATTATG ACTCAAATCA

3241 GTCTCCCCAA GCATTCGGGG ATCAGAGTTT TTAAGGATAA CTTAGTGTGT AGGGGGCCAG TGAGTTGGAG

3311 ATGAAAGCGT AGGGAGTCGA AGGTGTCTTT TTGCGCCGAG TCAGTTCCTG GGTGGGGGCC ACAAGATCGG

3381 ATGAGCCAGT TTATCAATCC GGGGGTGCCA GCTGATCCAT GGAGTGCAGG GTCTGCAAAA TATCTCAAGC

3451 ACTGATTGAT CTTAGGTTTT ACAATAGTGA TGTTACCCCA GGAACAATTT GGGGAAGGTC AGAATCTTGT

3521 AGCCTGTAGC TGCATGACTC CTAAACCATA ATTTCTTTTT TGTTTTTTTT TTTTATTTT TGAGACAGGG

PstI (3639)

3591 TCTCACTCTG TCACCTAGGC TGGAGTGCAG TGGTGCAATC ACAGCTCACT GCAGCCCTTA GAGCGGCGCG

3661 CACCGCGGTG GAGCTCCAAT TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTCG TTTTACAACG

3731 TCGTACTGCG GAAAACCCCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT CGCCAGCTGG

3801 CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC GAATGGCGCG

3871 AAATTGTAAA CGTTAATATT TTGTTAAAT TCGCGTTAAA TTTTGTAA ATCAGCTCAT TTTTAAACCA

3941 ATAGGCCGAA ATCGGCAAAA TCCCTTATAA ATCAAAAGAA TAGACCGAGA TAGGGTTGAG TGTGTGTTCA

4011 GTTTGGAACA AGAGTCCACT ATTAAGAAGC GTGGACTCCA ACGTCAAAGG GCGAAAACCC GTCTATCAGG

4081 GCGATGGCCC ACTACGTGAA CCATCACCCT AATCAAGTTT TTTGGGGTCG AGGTGCCGTA AAGCACTAAA

4151 TCGGAACCCCT AAAGGGAGCC CCCGATTAG AGCTTGACGG GGAAAGCCGG CGAACGTGGC GAGAAAGGAA

4221 GGGAGAGAAAG CGAAAGGAGC GGGCGCTAGG GCGCTGGCAA GTGTAGCGGT CACGCTGCGC GTAACCAACA

4291 CACCGCCCGC GCTTAATGCG CCGCTACAGG GCGCGTCCCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA

4361 ACCCTATTT GTTTATTTTT CTAAATACAT TCAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA

Fig. 14 C

continued

4431 TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT  
 4501 TCGGGCATT TGCCTTCCTG TTTTGTCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG  
 4571 TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCCGCCCCG  
 4641 AAGAACGTTT TCCAATGATG AGCACTTTTA AAGTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC  
 4711 CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA  
 4781 GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA  
 4851 CTGGCGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG  
 4921 GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGAC  
 4991 ACCACGATGC CTGTAGCAAT GGCAACAACG TTGCGCAAAC TAITAACTGG CGAACTACTT ACTCTAGCTT  
 5061 CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAAGGACCA CTTCTGCGCT CGGCCCTTCC  
 5131 GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG  
 5201 GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC  
 5271 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTGAGACC AAGTTTACTC  
 5341 ATATATACCT TAGATTGATT TAAAACTTCA TTTTAAATT AAAAGGATCT AGGTGAAGAT CCTTTTGTAT  
 5411 AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTTC ACTGAGCGTC AGACCCCGTA GAAAAGATCA  
 5481 AAGGATCTTC TTGAGATCCT TTTTCTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC  
 5551 AGCGGTGGTT TGTTTGCCGG ATCAAGAGCT ACCAACTCT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG  
 5621 CAGATACCAA ATACTGTCTT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAAGTCT GTAGCACCAG  
 5691 CTACATACCT CGCTCTGCTA ATCCTGTGAC CAGTGGCTGC TGCCAGTGGC GATAAGTCTG GTCTTACCGG  
 5761 GTTGGAAGCA AGACGATAGT TACCGGATAA GGCAGCGCGG TCGGGCTGAA CGGGGGGTTT GTGCACACAG  
 5831 CCCAGCTTGG AGCGAAGGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC  
 5901 TTCCCGAAGG GAGAAAGCGG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA  
 5971 GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCTGA  
 6041 TTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT TTACGGTTCC  
 6111 TGGCCCTTTG CTGGCCTTTT GCTCACATGT TCCTTCCTGC GTTATCCCTT GATTCTGTGG ATAACCGTAT  
 6181 TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG  
 6251 GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCAATTA TGCAGTTGGC  
 6321 ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTAGC TCACTCATT  
 6391 GGCACCCAG GCTTTACTT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT  
 6461 CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTCG GAATTAACCC TCACTAAAGG GAACAAAAGC  
 PstI (6533)  
 6531 TGCTGCAGGG TCCCTAACTG CCAAGCCCCA CAGTGTGCCC TGAGGCTGCC CCTTCCTTCT AGCGGCTGCC  
 6601 CCCACTCGGC TTTGCTTTCC CTAGTTTCAG TTACTTGGCT TCAGCCAAGG TCTGAAACTA GGTGCGCACA  
 6671 GAGCGGTAAG ACTGCGAGAG AAAGAGACCA GCTTTACAGG GGGTTTATCA CAGTGACCCC TGACAGTCGT  
 6741 CAGCCTCACA GGGGGTTTAT CACATTGCAC CCTGACAGTC GTCAGCCTCA CAGGGGGTTT ATCAGAGTGC  
 6811 ACCCTTACAA TCATTCCATT TGATTACAAA TTTTTTGTAG CTCTACTGTG CCTAACTTGT AAGTTAAATT  
 6881 TGATCAGAGG TGTGTTCCCA GAGGGGAAAA CAGTATATAC AGGGTTCAGT ACTATCGCAT TTCAGGCCTC  
 6951 CACCTGGGTC TTGGAATGTG TCCCCGAGG GGTGATGACT ACCTCAGTTG GATCTCCACA GGTACAGTGC  
 7021 ACACAAGATA ACCAAGACAC CTCCCAAGGC TACCACAATG GGCCGCCCTC CACGTGCACA TGGCCGGAGG  
 7091 AACTGCCATG TCGGAGGTGC AAGCACACCT GCGCATCAGA GTCCTTGGTG TGGAGGGAGG GACCAGCGCA  
 7161 GCTTCCAGCC ATCCACCTGA TGAACAGAAC CTAGGGAAAG CCCAGTTCT ACTTACACCA GGAAGGCG

Fig. 14 D